



## EXHIBIT A

### 1. SEQ5 vs. SEQ2

Aligned Length = 81    Gaps = 1  
Identities = 45 (55%)    Similarities = 12 (14%)

```
SEQ5 1 MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNST 50
SEQ2 1 MRLALSGLLCMLLLCFCIFSSEGRRHPAKSLKLRR---CCHLSPRSKLT 47
      **** * * * * . * * * * . * * . * * . * * . * * * * * * * *
```

```
SEQ5 51 NLKGHHVRLCKPCKLEPEPRLWVVP GALPQV 81
SEQ2 48 TWKGNHTRPCR LCRNKL PVKSWVVP GALPQI 78
      . * * . * * * . * . * * * * * .
```

### 2. SEQ5 vs. SEQ7

Aligned Length = 81    Gaps = 2  
Identities = 38 (46%)    Similarities = 11 (13%)

```
SEQ5 1 MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNST 50
SEQ7 1 MRLTL SGLFFMLFLCLCVLSSEGRKRP AKFPKLRP---RCHLSPRSKPI 47
      **** * * * . * * * . . * . * * . * * * * * * * * * *
```

```
SEQ5 51 NLKGHHVRLCKPCKLEPEPRLWVVP GALPQV 81
SEQ7 48 TWKGNHTRPCR PCR-KLESNSWVVP GALPQI 77
      . * * . * * * . * . * * * * * .
```